

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:15:58 ; Search time 172.18 Seconds
(without alignments)
221.041 Million cell updates/sec

Title: US-09-052-089a-3
Perfect score: 1066
Sequence: 1 RTIINKLFFDLAQBEEENVLD.....DLQSADEKIMSLKKRLTMLQ 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1066	100.0	469	4	000467
2	1046	98.1	469	4	Q9BWP2
3	919	86.2	470	11	Q9CWP4
4	919	86.2	470	11	Q08854
5	654	61.4	233	13	Q922M8
6	530	49.7	433	13	Q9YGN2
7	178	16.7	1958	5	Q96062
8	167	15.7	529	4	Q9UP81
9	167	15.7	948	4	Q9UIK7
10	167	15.7	2473	11	Q9Q284
11	165	15.5	1092	13	Q90338
12	165	15.5	1578	10	Q9AV25
13	165	15.5	1931	13	Q42352
14	164.5	15.4	324	11	Q9EGN8
15	164	15.4	692	5	Q96720
16	164	15.4	1530	4	Q43241

17	163	15.3	1933	13	Q90337	Q90337 cyprinus ca
18	162	15.2	976	11	Q99M12	Q99M12 mus musculu
19	162	15.2	1120	11	Q99M11	Q99M11 mus musculu
20	162	15.2	1743	5	Q96063	Q96063 dugesia jap
21	162	15.2	1930	13	Q9B6D5	Q9B6D5 pennahia ar
22	161	15.1	1447	11	Q9QY72	Q9QY72 mus musculu
23	161	15.1	1487	11	Q9QY73	Q9QY73 mus musculu
24	160.5	15.1	876	5	Q9BWM8	Q9BWM8 sarcopites s
25	160.5	15.1	1219	5	Q9NJ23	Q9NJ23 aequipecten
26	160.5	15.1	2168	11	Q61043	Q61043 mus musculu
27	160	15.0	435	5	Q95S85	Q95S85 drosophila
28	159.5	15.0	1229	5	Q9NJ22	Q9NJ22 aequipecten
29	159.5	15.0	1243	5	Q9NJ21	Q9NJ21 aequipecten
30	159.5	15.0	1253	5	Q9NJ20	Q9NJ20 aequipecten
31	159.5	15.0	1951	5	Q17042	Q17042 aequipecten
32	159.5	15.0	2139	5	Q07569	Q07569 entamoeba h
33	159	14.9	1790	3	Q07380	Q07380 saccharomyc
34	159	14.9	1939	6	Q9TV61	Q9TV61 sus scrofa
35	158.5	14.9	1941	5	Q26079	Q26079 placopecten
36	156.5	14.7	786	13	Q91520	Q91520 thunnus thy
37	156.5	14.7	1138	5	Q22276	Q22276 caenorhabdi
38	156.5	14.7	1940	5	Q9U7E3	Q9U7E3 pecten maxi
39	155.5	14.6	959	11	Q91WE7	Q91WE7 mus musculu
40	155.5	14.6	1164	5	P92021	P92021 caenorhabdi
41	155.5	14.6	1205	5	Q967H0	Q967H0 caenorhabdi
42	155.5	14.6	1935	5	Q44934	Q44934 loligo peal
43	155.5	14.6	1938	13	Q91BD7	Q91BD7 seriola dum
44	155	14.5	1455	5	Q9V8D7	Q9V8D7 drosophila
45	155	14.5	1119	13	P87344	P87344 theragra ch

ALIGNMENTS

RESULT 1
ID 000467 PRELIMINARY: PRT: 469 AA.
AC 000467;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HTRIP.
GN HTRIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RX MEDLINE=97258620; PubMed=9104814;
RA Lee S.Y., Lee S.Y., Choi Y.;
RT "TRAF-interacting protein (TRIP): a novel component of the tumor
RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
RT that inhibits TRAF2-mediated NF-kappaB activation.";
RC J. Exp. Med. 185:1275-1285(1997).
CL -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: U77845; AAB52993.1;
DR InterPro: IPR001841; ZnfC1ng.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 469 AA; 53138 MW; 2D54ED04B84ABAE4 CRC64;

Query Match 100.0%; Score 1066; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 1,le-52;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTIINKLFFDLAQBEEENVLDREPLKNELNDVRAOLSKDKKRSQVITDRLPTLEERN 60
DB 56 RTIINKLFFDLAQBEEENVLDREPLKNELNDVRAOLSKDKKRSQVITDRLPTLEERN 115
QY 61 ATVVSLOALGKAMWLSTLKKOMKYLEQOQDETQAOEAGRLRSKKMTMEQIELLOS 120

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Db 116 ATVYSIQALKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLSKKMTMEQIELLQS 175
QY 121 QLPVEEEMIRMGVQGSVEQOLAVYCVSLKKEYENLKARRKASGVADKLKRDLFSSRSK 180
Db 176 QLPVEEEMIRMGVQGSVEQOLAVYCVSLKKEYENLKARRKASGVADKLKRDLFSSRSK 235
QY 181 LQTVYSELDOAKLELKSQKDLQSDAKREIMSLKKLTMLQ 220
Db 236 LQTVYSELDOAKLELKSQKDLQSDAKREIMSLKKLTMLQ 275

RESULT 2
Q9BMF2 PRELIMINARY: PRT: 469 AA.
AC Q9BMF2:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TRAF INTERACTING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC000310; AAH00310.1; -.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 469 AA; 53294 MW; B9EF3808BFC5985B CRC64;

Query Match 98.1%; Score 1046; DB 4; Length 469;
Best Local Similarity 98.6%; Pred. No. 1.4e-51;
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 RTIINKLFFDLQAEENVLDBREFLNELNDVNRQOLSQDKRKRSQVITDRLRPLEERN 60
Db 56 RTIINKLFFDLQAEENVLDBREFLNELNDVNRQOLSQDKRKRSQVITDRLRPLEERN 115
QY 61 ATVYSIQALKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLSKKMTMEQIELLQS 120
Db 116 ATVYSIQALKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLSKKMTMEQIELLQS 175
QY 121 QLPVEEEMIRMGVQGSVEQOLAVYCVSLKKEYENLKARRKASGVADKLKRDLFSSRSK 180
Db 176 QLPVEEEMIRMGVQGSVEQOLAVYCVSLKKEYENLKARRKASGVADKLKRDLFSSRSK 235
QY 181 LQTVYSELDOAKLELKSQKDLQSDAKREIMSLKKLTMLQ 220
Db 236 LQTVYSELDOAKLELKSQKDLQSDAKREIMSLKKLTMLQ 275

RESULT 3
Q9CPA4 PRELIMINARY: PRT: 470 AA.
AC Q9CPA4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TRAF INTERACTING PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=9258620; PubMed=9104814;
RA Lee S.Y., Lee S.Y., Choi Y.;
DE "TRAF-interacting protein (TRIP): a novel component of the tumor

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Balow S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AK012948; BAB28567.1; -.
DR EMBL; AK012786; BAB28469.1; -.
DR MGD: MGI:1096377; Traip.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 470 AA; 53149 MW; EBFABC49A9F4BFEZ CRC64;

Query Match 86.2%; Score 919; DB 11; Length 470;
Best Local Similarity 85.5%; Pred. No. 1.9e-44;
Matches 188; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
QY 1 RTIINKLFFDLQAEENVLDBREFLNELNDVNRQOLSQDKRKRSQVITDRLRPLEERN 60
Db 56 RTIINKLFFDLQAEENVLDBREFLNELNDVNRQOLSQDKRKRSQVITDRLRPLEERN 115
QY 61 ATVYSIQALKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLSKKMTMEQIELLQS 120
Db 116 ATVYSIQALKAEMLCSTLKKOMKYLEQOODETKQAOEAGRLSKKMTMEQIELLQS 175
QY 121 QLPVEEEMIRMGVQGSVEQOLAVYCVSLKKEYENLKARRKASGVADKLKRDLFSSRSK 180
Db 176 QLPVEEEMIRMGVQGSVEQOLAVYCVSLKKEYENLKARRKASGVADKLKRDLFSSRSK 235
QY 181 LQTVYSELDOAKLELKSQKDLQSDAKREIMSLKKLTMLQ 220
Db 236 LQTVYSELDOAKLELKSQKDLQSDAKREIMSLKKLTMLQ 275

RESULT 4
Q00854 PRELIMINARY: PRT: 470 AA.
AC Q00854:
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MTRIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=9258620; PubMed=9104814;
RA Lee S.Y., Lee S.Y., Choi Y.;
DE "TRAF-interacting protein (TRIP): a novel component of the tumor

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RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
 RT that inhibits TRAF2-mediated NF-kappaB activation.";
 RL J. Exp. Med. 185:1275-1285(1997).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: U77844; AAB52994.1; -.
 DR MGD: MGI:1096377; Trafp.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 470 AA; 53191 MW; 00FD705B52645133 CRC64;

Query Match 86.2%; Score 919; DB 11; Length 470;
 Best Local Similarity 85.5%; Pred. No. 1.9e-44;
 Matches 188; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 RTIINKLFEDLAQEEENVLDREFLKNEIDNVRAQLSQDKRKRSQVIITDLRTLEERN 60
 :|||||
 Db KTIINKLFEDLAQEEENVLDREFLKNEIDSVKQLSQDKRKRSQAIITDLRTLEERN 115
 QY 61 ATVVSLOALGKAEMLGSLTKKMKYLEQODETKQAQEEAGRLRSKKTMEQIEILLQS 120
 :|||||
 Db ATVESLQALNKAEMLSLTKKMKFLEQRQDETKQAAREEAHRLCKKKTMEQIEILLQS 175
 QY 121 QLPVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKARKASGEVADKLKKDLFFSSRSK 180
 :|||||
 Db 176 QRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKARKATGETLADRLKDLVSSRSK 235
 QY 181 LQTVYSELDAQKLELSAQKDLQSAQDKREIMSLKKRLMLQ 220
 :|||||
 Db LKTLNTELDQAKLELSAQKDLQSAQDEITSLRKKLMLQ 275

RESULT 5
 Q922M8 PRELIMINARY; PRT; 223 AA.
 AC Q922M8;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TRAF-INTERACTING PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC006929; AAH06929.1; -
 SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match 61.4%; Score 654; DB 11; Length 223;
 Best Local Similarity 88.7%; Pred. No. 6.6e-30;
 Matches 134; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RTIINKLFEDLAQEEENVLDREFLKNEIDNVRAQLSQDKRKRSQVIITDLRTLEERN 60
 :|||||
 Db KTIINKLFEDLAQEEENVLDREFLKNEIDSVKQLSQDKRKRSQAIITDLRTLEERN 115
 QY 61 ATVVSLOALGKAEMLGSLTKKMKYLEQODETKQAQEEAGRLRSKKTMEQIEILLQS 120
 :|||||
 Db ATVESLQALNKAEMLSLTKKMKFLEQRQDETKQAAREEAHRLCKKKTMEQIEILLQS 175
 QY 121 QLPVEEMIRDMGVGQSAVEQLAVYCVSLK 151
 :|||||
 Db 176 QRSEVEEMIRDMGVGQSAVEQLAVYCVSLK 206

RESULT 6
 Q9YGN2 PRELIMINARY; PRT; 433 AA.
 AC Q9YGN2;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TRAF INTERACTING PROTEIN.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99148833; PubMed-10025966;
 RA Coclague A.J., Clark M., Hawker K., Umranta Y., Wheller D., Bishop M.,
 RA Elgar G.;
 RT "Three receptor genes for plasmidogen related growth factors in the
 RT genome of the puffer fish Fugu rubripes.";
 RL FEBS Lett. 443:370-374(1999)
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AB010317; CA409084.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;

Query Match 49.7%; Score 530; DB 13; Length 433;
 Best Local Similarity 47.3%; Pred. No. 1.1e-22;
 Matches 104; Conservative 53; Mismatches 63; Indels 0; Gaps 0;

QY 1 RTIINKLFEDLAQEEENVLDREFLKNEIDNVRAQLSQDKRKRSQVIITDLRTLEERN 60
 :|||||
 Db RHIIISRLTFDVLDDSDGDEPSLQNEIDRVKVNFSKREKQKAMDLMETVELR 115
 QY 61 ATVVSLOALGKAEMLGSLTKKMKYLEQODETKQAQEEAGRLRSKKTMEQIEILLQS 120
 :|||||
 Db KALENLQDVMEKELCSALTQMTYLESQHNDRPAAAEVRRIRIKKKTESLDVVLQ 175
 QY 121 QLPVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKARKASGEVADKLKKDLFFSSRSK 180
 :|||||
 Db 176 QRAVESMITDMGICQAAVEQLSTYICISLKKEYENLKAGKSSNMCKLRKREYVTSNNK 235
 QY 181 LQTVYSELDAQKLELSAQKDLQSAQDKREIMSLKKRLMLQ 220
 :|||||
 Db LHKALLELTAKARDPMKSLQNDLTNAKEISSLKKVEFLQ 275

RESULT 7
 Q96062 PRELIMINARY; PRT; 1958 AA.
 AC Q96062;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 GN DJMHC-A.
 OS Dugesia japonica (Planarian).
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
 OC Paludicola; Dugesidae; Dugesia.
 OX NCBI_TaxID=6161;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kobayashi C., Kobayashi S., Orli H., Agata K., Watanabe K.;
 RT "Identification of two distinct muscles in the planarian, Dugesia
 RT japonica, by the expression of myosin heavy chain genes.";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB015484; BAA34954.1; -.
 DR HSSP: P24733; IWDG.
 DR InterPro: IPR001064; Crystallin.


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RESULT 13
042352 PRELIMINARY: PRT: 1931 AA.
AC 042352:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RX MEDLINE=97352533; PubMed=9208928;
RA Htayama Y., Matabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RT muscle.";
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL; D89991; BAA22068.1; -.
DR HSSP; P13538; ZMYS.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
SQ SEQUENCE 1931 AA; 221162 MW; 5946687BD0872DDD CRC64;

Query Match 15.5%; Score 165; DB 13; Length 1931;
Best Local Similarity 23.1%; Pred. No. 0.14;
Matches 59; Conservative 49; Mismatches 87; Indels 60; Gaps 8;

QY 15 EENVLDREF-----LKNELDVNRQLSQDKRKRSOYIIDLRTLEER 59
DB 1177 EESTLQHTATAALAKKQADVAELGEIDNLQKRYKQLEKESYKMEIDDTISNME-- 1234
QY 60 NATVSLQOALGKAEMLCSTLKQKKYLEQOODETKQAQEEAGRLSRKMT-----M 111
DB 1235 -----AVAKAGNLEKMCRTLEDQLSEIKAKSDENSRQLDNMNQARLQTENGEFSHQL 1289
QY 112 EQIELLOSQRP-----EVEEMIRDMGCGSAVEDLAVYCVSLKKEYENL 156
DB 1290 EEKALV-SQLTRGKAFTQOIEDLRHVEEVKAKNALAHAVOSARHCDLLRQYEEB 1348
QY 157 KEAR-----KASGEVAD---KLKRDLPSSRSKLQTVSELDQAKLELSAOKDLQSA 205
DB 1349 QEATLEQORGSKANSEVAQNRAKYETDAIOTTELEBAKKKLAAO---RLQDAEESIAV 1405
QY 206 DKEIMSLKKKLTLMLQ 220
DB 1406 SSKCASLEKTKQRLQ 1420

RESULT 14
Q9EON8 PRELIMINARY: PRT: 324 AA.
AC Q9EON8:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MITOSIN (FRAGMENT).
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Qian M., Lin D., Zhu X.;
RT "Evolution of the internal repeat of mtosin."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF182407; AAC63426.1; -.
DR InterPro; IPR000533; Tropomyosin.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 1 1
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 37896 MW; AC4CD5A55EIDPFD7D CRC64;

Query Match 15.4%; Score 164.5; DB 11; Length 324;
Best Local Similarity 22.5%; Pred. No. 0.027;
Matches 54; Conservative 55; Mismatches 98; Indels 33; Gaps 4;

QY 4 INKLFPLAOEEN-----VLDRFLKNELDVNRQLSQDKRKRSOYIIDLRTLEER 59
DB 28 VENLERLEEMSENOELAILDSENLKAEVETLKAQMDMAKSLRVFELDLNVNSERENL 87
QY 60 NATVSLQOALGKAEMLCSTLKQKKYLEQO-----ODETKQAQEEAGRL 104
DB 88 AKQLOEKRSRVSLEDELCSLSRLSSEKQARVQMERKRSAMLMQLQKLEIMEVAL 147
QY 105 RSKMKTMEQIELLOSQLPVEVEEMIRDMGCGSAVEQLAVYCVSLKKEYENLEAKRAGS 164
DB 148 YNDDETLKAQOSLDQPEEVHLL-----KSSIQKLVHIDADKKKQCHILEQLKESK 200
QY 165 EVAD-----KLKRDLPSSRSKLQTVSELDQAKLELSAOKDLQSDKREIMSLKKLT 217
DB 201 HHADLFKRVENLEELMLSEKKNKHLLEQAENSKAETQTLTKETQMDNLQDLELELT 260

RESULT 15
Q96720 PRELIMINARY: PRT: 692 AA.
AC Q96720:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PARAMYOSIN-LIKE ALLERGEN (FRAGMENT).
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcophthiformes; Astigmata; Analgoidea; Pyroglyphidae;
OC Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98389068; PubMed=9723675;
RA Tsai L.C., Chao P.L., Shen H.D., Tang R.B., Chang T.C., Chang Z.N.,
RA Hung M.W., Lee B.L., Chua K.Y.;
RT "Isolation and characterization of a novel 98-kD Dermatophagoides
RT farinae mite allergen."
RL J. Allergy Clin. Immunol. 102:295-303(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20062524; PubMed=10594536;
RA Tsai L., Sun Y., Chao P., Ng H., Hung M., Hsieh K., Liaw S., Chua K.;
RT "Sequence analysis and expression of a cDNA clone encoding a 98-kDa
RT allergen in Dermatophagoides farinae."
RL Clin. Exp. Allergy 29:1606-1613(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Tsai L.-C., Chao P.-L., Ng H.-P., Chua K.-Y.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF352244; AAK39511.1; -.
FT NON_TER 692 692
SQ SEQUENCE 692 AA; 81372 MW; 61FC6380C9D7C9E2 CRC64;
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Query Match 15.4%; Score 164; DB 5; Length 692;
Best Local Similarity 22.1%; Pred. No. 0.06;
Matches 65; Conservative 63; Mismatches 78; Indels 88; Gaps 11;

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QY 4 INKLEFPDIA-----OEENVLNDEEF--LNKNELDN---VAALQISO-----KQKEX 42
Db 104 INRVIVELTSHKQKOLSCOEENVELLKEVHEVUKIQLDNANHMKITQIAQOULEDTNRHRLBEEBK 163
QY 43 RDS-----QVIIDPLRDLTLEERNATVYSLQALGKA-----73
Db 164 RASLENNHAHTLEVELESITKVLQDDEESARLELEBQITRKANDASWKSXYEALQAHAD 223
QY 74 -----EML-----GSLTKKQMYLLEQOD-----ERKQOQEEGRGRSK 107
Db 224 VEELRRKMAQITSEYEOLLEALLNKCSGLEQKSRLOSEVEVYLIMDELEKTRRHQOULEKR 283
QY 108 MKTMEQIETELLQSOLPEVEEMIRDMGVGQSAVEQOLAYCVYSLKK--EYENLKBEARRASG 164
Db 284 VAOLEKIMLIDKNKLEEYTYMIM-----EQNQKELRYKIAELQKQLQHEYERUKLRDQOQLA 337
QY 165 EVAQKLRKLEDSRSSKIQOTVYSELDQAKKLELK---SAQKDLQSDKREIMSLKXK 215
Db 338 RENKKTLDLLEAKSSQLDANDARRIRHBEQIETIKRLNRENEDEDSAAVYKAEITLRKO 391

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RESULT	16			
043241				
ID	043241	PRELIMINARY;	PRT;	1530 AA.
AC	043241;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	GGP170.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97442456; PubMed=9295333;			
RA	Misumi Y., Sohda M., Yano A., Fujiwara T., Ikehara Y.;			
RT	"Molecular Characterization of GGP170, a 170-kDa Protein Associated			
RT	with the Cytoplasmic Face of the Golgi Membrane.";			
RL	J. Biol. Chem. 272:23851-23858(1997).			
EMBL	D63197; BA423661.1.			
QQ	SEQUENCE 1530 AA; 170068 MW. E3851F2ABFA1A533 CRC64;			

Query Match	15.48;	Score 164;	DB 4;	Length 1530;
Best Local Similarity	25.08;	Pred. No. 0.13;		
Matches	60;	Conservative 46;	Mismatches 96;	Indels 38;
			Gaps	7

QY	13	QEEENVLDREFLKEILD-----NVRNOLSOXKKEKRDQSQVILIDTLDLTERNRNTVYSL	66
Db	1132	REHNSIETALAKREADLYVNLQVAVIOLKEEDBROKHVLQVLAQVSLERKEKRVSL	1191
QY	67	QOALGAEMLCSTLKMKOMKYLEOODETK-----QAOEAGRLSRKKKATHE-	112
Db	1192	KEQVAAAKVLEAGNHRIRFKFASLELSYVKKELOAKHLVYKIQAEKDDIQITREGRHSQEI	1251
QY	113	---QIEL-----LIQSOLFVEEEMIRDMVGOSAVBQLAVVYCVSLKREYENLKEARK	161
Db	1252	AQOFAELAEARAOHLOLLOKOL---DEQLSKPQNGNOMENMLKWEYDQKRETIQSLKOULD	1308
QY	162	ASGEVAQKLRLDESSKSKIQTYVSELDQAKKLELSAQNDQDSADKELMSLKKKL-TMQL	220
Db	1309	LTEQOG---KELEGILOQDILLQNVKSELEMAQDELSTMQDKDFMLQAKVSLKNNKMTLQI	1365

RESULT 17
Q90337

ID	Q90337	PRELIMINARY;	PRT;	1933 AA.
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DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_taxid=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST SKELETAL MUSCLE;
RX MEDLINE=97352533; PubMed=9208928;
RA Hirayama Y., Matabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RT muscle."
RL Eur. J. Biochem. 246:380-387(1997).
RN [2]
RP SEQUENCE OF 738-1933 FROM N.A.
RC TISSUE=FAST SKELETAL MUSCLE.
RX MEDLINE=97176447; PubMed=9023993;
RA Imai Y., Hirayama Y., Kikuchi K., Kakinuma M., Matabe S.;
RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
RT muscle and their gene expression associated with temperature
RT acclimation."
RL J. Exp. Biol. 200:27-34(1997).
DR EMBL: D88990; BAA22067.1; -
DR EMBL: D50474; BAA09067.1; -
DR HSSP: P1538; ZMY5.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR InterPro: IPR002928; myosin_tall.
DR Pfam: PF00612; IQ: 1.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; myosin_N; 1.
DR Pfam: PF01576; myosin_tall; 1.
DR PRINTS: PD00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ: 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PSS0096; IQ; 1.
KW Myosin.
SQ SEQUENCE 1933 AA: 221092 MW: 255305 CRC64:

```

Query Match	15.3%;	Score 163;	DB 13;	Length 1933;
Best Local Similarity	23.1%;	Pred. No. 0.18;		
Matches	59;	Conservative	50;	Mismatches 86;
			Indels	60;
			Gaps	8

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0Y 15 EENVUDREF-----LNELNDVNAQOLSOQDKREKRSQVYIDTIRLTLEER 59
Db 1178 EESTIQEHATVATLARKKOADSVAELGBQIDNLOIRIKOLEKERSSEKKEIDLSSNME-- 12355
0Y 60 NATVSLQOALGKAEMCSTLKKQMKYLEQOQOQDETQAOEAGRLRSKMT-----M 111
Db 1236 -----AVAKKAGNLEKMCRTLEQDLSLTKAKKSSENRQLDNMNAQRARLQTFENGFSRQL 1290
0Y 112 EOEILLLOSQLP-----EVEEMIRDMGVQOQSAVEOLAYVCSLKEVEYNL 156
Db 1291 EEKEKLV-SQLTRGKQAFQOQIEDLKRHVEEYKAKNALAHAVQASRHDCDLREQYEE 1349
0Y 157 KEAR-----KASGEVAD--KLKRDLPSSRSKIQTVYSELDOAKLELKSQDKLOSA 205
Db 1350 QEAKNELOQKMSKANSEVAQWAPRAKYEYDALQIREELLESKKLQAG--RLQDAEESITAV 1406
0Y 206 DKEIMSLKKKLITMLQ 220
Db 1407 NSKCASTLEKTKORLO 1421

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RESULT	23		
09QY73			
ID	09QY73	PRELIMINARY;	PRT: 1487 AA.
AC	09QY73;		
DT	01-MAY-2000 (TREMBLrel, 13, Created)		
DT	01-OCT-2001 (TREMBLrel, 18, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)		
DE	MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3.		
GN	MEK2/GOLGA3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL6;		
RA	Matsukuma S.;		
RT	"Meak2/Golga3 Gene Product Is Indispensable for Spermatogenesis In the		
RL	Mouse.";		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AB029537: BAA86889.2: -	JOINED	
DR	EMBL: AB029521: BAA86889.2: -	JOINED	
DR	EMBL: AB029522: BAA86889.2: -	JOINED	
DR	EMBL: AB029523: BAA86889.2: -	JOINED	
DR	EMBL: AB029524: BAA86889.2: -	JOINED	
DR	EMBL: AB029525: BAA86889.2: -	JOINED	
DR	EMBL: AB029526: BAA86889.2: -	JOINED	
DR	EMBL: AB029527: BAA86889.2: -	JOINED	
DR	EMBL: AB029528: BAA86889.2: -	JOINED	
DR	EMBL: AB029529: BAA86889.2: -	JOINED	
DR	EMBL: AB029530: BAA86889.2: -	JOINED	
DR	EMBL: AB029531: BAA86889.2: -	JOINED	
DR	EMBL: AB029532: BAA86889.2: -	JOINED	
DR	EMBL: AB029533: BAA86889.2: -	JOINED	
DR	EMBL: AB029534: BAA86889.2: -	JOINED	
DR	EMBL: AB029535: BAA86889.2: -	JOINED	
DR	EMBL: AB029536: BAA86889.2: -	JOINED	
Q0	SEQUENCE 1487 AA: 167175 MW: 58ADP716C251FBFF CRC64;		

Query Match	15.18	Score	161	DB	11	Length	1487
Best Local Similarity	23.18	Pred. No.	0.18				
Matches	57	Conservative	48	Mismatches	90	Indels	52
						Gaps	7

QY	13	OEENVAIDREFLNKELD-----NVAOLSOJKREKRSOVSIIIDPLOTBERNRNTVSL	66
Dd	1128	RENHSIETALAKREADDVLONLNOVALORKEEBEROKOLVOALOVSLEKEMEVNSL	1187
QY	67	QOALGKA-----EMLSTLKOMKYULEOO-----ODET	94
Dd	1188	KEOAARAEAGHNRHRFKATLETSEVKELQACHLVOTLODAVEDELQIDOGKHSGEI	1247
QY	95	KAOEEGRILRSKMKTMEQTEJLLLOSOLPREVEMITDMGVGSANVEOLAVYSLSKKEYE	154
Dd	1248	AOFETLAEARTOLO-----LLOKKRL--BEOMSOPRTGSOMEEDKLWELDOKERETO	1297
QY	155	NLKEARKASGEVDKLRKDLFSSRSRIQTVYSELDAQLETLSAKOARDLOSADKEIMSLSK	214
Dd	1298	SIRKOQDUJTFEQOG---KKELEGTOITLOTTIKSELEAVOEDLSFTQDKDFMIAQAKSELKN	1354
QY	215	KL-TMLO 220 : :	
Dd	1355	NMKTLLO 1361 : :	

RESULT	24	
Q9BMM8		
ID	Q9BMM8	PRELIMINARY;
AC	Q9BMM8	PRT; 876 AA.
DT	01-JUN-2001	(REMBLrel. 17, Created)
DT	01-JUN-2001	(REMBLrel. 17, Last sequence update)
DT	01-DEC-2001	(REMBLrel. 19, Last annotation update)
DE	PARAYOSIN.	

OS Sarcophiles scabiei.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptriformes; Astigmata; Sarcoptridea; Sarcoptridae;
OC Sarcophiles.
XX NCBI_TaxID=52283;
RN [1]
RP SEQUENCE FROM N.A.
RA Mattsson J.G., Ljunggren E.L., Bergstrom K.;
RT "Parasitism from the parasitic mite Sarcophiles scabiei: cDNA cloning
RT and heterologous expression.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF317670; AAR01181.1; -
DR InterPro: IPR002928; Myosin_tall.
DR InterPro: IPR001854; Ribosomal_L29.
DR Pfam: PF01576; Myosin_tall.1.
SQ SEQUENCE 876 AA; 102454 MW; C99475EE7A0DAE52 CRC64;

Query Match	15.1%	Score 160.5;	DB 5;	Length 876;
Best Local Similarity	24.6%	Pred. No. 0.12;		
Matches 64;	Conservative 49;	Mismatches 90;	Indels 57;	Gaps 9

[illegible]

RESULT	25	
Q9NJ23		
ID	Q9NJ23	PRELIMINARY;
AC	Q9NJ23;	PRT; 1219 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-DIC-2001 (TREMBLrel. 19, Last annotation update)	
DE	MYOSIN HEAVY CHAIN STRINTED MUSCLE SPECIFIC ISOFORM (FRAGMENT).	
GN	MHC.	
OS	Aequiptecten irradians (Bay scallop).	
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;	
OC	Pectinoidea; Pectinidae; Argopecten.	
OX	NCBI_TaxID=31199;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=200090924; PubMed=10623517;	
RA	Yamada A., Yoshio M., Owa K., Nityray L.;	
RT	"Catching, a novel protein in molluscan catch muscles, is produced by	
RT	alternative splicing from the myosin heavy chain gene.";	
RL	J. Mol. Biol. 295:169-178(2000).	
DR	EMBL: AF183909; AAF62391.1; -.;	
DR	HSSP: P24733; IMDC.	
DR	InterPro: IPR000048; IQ.	
DR	InterPro: IPR001609; myosin_head.	
DR	InterPro: IPR002928; myosin_tail.	
DR	InterPro: IPR002017; Spectrin.	
DR	InterPro: IPR000533; Tropomyosin.	
DR	Pfam: PF00612; IQ. 2.	
DR	Pfam: PF00063; myosin_head. 1.	
DR	Pfam: PF01576; myosin_tail. 1.	

RA Yamada A., Yoshio M., Olwa K., Nyitray L.;
RT "Catchin, a novel protein in molluscan catch muscles, is produced by
RT alternative splicing from the myosin heavy chain gene.";
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909; AAF62392.1; -.
DR HSSP: P24733; IMDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR PROSITE: PS50096; IQ; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 1229 AA; 142180 MW; 1764276CB904FDC9 CRC64;

Query Match 15.0%; Score 159.5; DB 5; Length 1229;
Best Local Similarity 27.4%; Pred. No. 0.19; Mismatches 75; Indels 27; Gaps 7;
Matches 57; Conservative 49;

QY 10 DLAGEENVLDREFLKNEL-DNVR--AQLSQDKKRDQYIIDTLRDTLEERNATVYS 65
DB 336 DLKSTQENVEDERVKRELEENVRRKEAELSSLSKLEDEQVLVSQLORKIKELQARIEE 395
QY 66 LQALGKAEMLCSTLKKOMKYLEQOODETKQAQEEAGRLRSKMKTMEQIELLSQLPVEY 125
DB 336 LEEELAEARNARAKVEKQRAELRELELGERLDEAG-----ATSAQIELNKKRE-AEL 449
QY 126 EEMIDMGVGSABVQLAVVYCVSLKKEYENLKEARKAGEVADKLKDLFSSRSKLQTVY 185
DB 450 LKIRRDLD--EASLQHEAQISALRKHQD-----AANEMADQV-----DQLQVKV 492

QY 186 SELDQAKLELKSQKDLQSDAKETMSLK 213
DB 493 SKSEKEKQQLRSEVEDLQAQIOHISKNK 520

RESULT 29
Q9NJ21 PRELIMINARY; PRT; 1243 AA.
AC Q9NJ21;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 1 (FRAGMENT).
GN MHC.
OS Aequiptecten irradians (Bay scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
KM SEQUENCE FROM N.A.
RX MEDLINE=20090924; PubMed=10623517;
RA Yamada A., Yoshio M., Olwa K., Nyitray L.;
RT "Catchin, a novel protein in molluscan catch muscles, is produced by
RT alternative splicing from the myosin heavy chain gene.";
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909; AAF62394.1; -.
DR HSSP: P24733; IMDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR PROSITE: PS50096; IQ; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 1253 AA; 144774 MW; 56E4FF0226B58C92 CRC64;

DR SMART: SM00015; IQ; 1.
RT PROSITE: PS50096; IQ; 1.
FT NON_TER 1
SQ SEQUENCE 1243 AA; 143531 MW; B5C7219BF2B8AE CRC64;

Query Match 15.0%; Score 159.5; DB 5; Length 1243;
Best Local Similarity 27.4%; Pred. No. 0.19; Mismatches 75; Indels 27; Gaps 7;
Matches 57; Conservative 49;

QY 10 DLAGEENVLDREFLKNEL-DNVR--AQLSQDKKRDQYIIDTLRDTLEERNATVYS 65
DB 336 DLKSTQENVEDERVKRELEENVRRKEAELSSLSKLEDEQVLVSQLORKIKELQARIEE 395
QY 66 LQALGKAEMLCSTLKKOMKYLEQOODETKQAQEEAGRLRSKMKTMEQIELLSQLPVEY 125
DB 336 LEEELAEARNARAKVEKQRAELRELELGERLDEAG-----ATSAQIELNKKRE-AEL 449
QY 126 EEMIDMGVGSABVQLAVVYCVSLKKEYENLKEARKAGEVADKLKDLFSSRSKLQTVY 185
DB 450 LKIRRDLD--EASLQHEAQISALRKHQD-----AANEMADQV-----DQLQVKV 492

QY 186 SELDQAKLELKSQKDLQSDAKETMSLK 213
DB 493 SKSEKEKQQLRSEVEDLQAQIOHISKNK 520

RESULT 30
Q9NJ20 PRELIMINARY; PRT; 1253 AA.
AC Q9NJ20;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 2 (FRAGMENT).
GN MHC.
OS Aequiptecten irradians (Bay scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
KM SEQUENCE FROM N.A.
RX MEDLINE=20090924; PubMed=10623517;
RA Yamada A., Yoshio M., Olwa K., Nyitray L.;
RT "Catchin, a novel protein in molluscan catch muscles, is produced by
RT alternative splicing from the myosin heavy chain gene.";
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909; AAF62395.1; -.
DR HSSP: P24733; IMDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR PROSITE: PS50096; IQ; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 1253 AA; 144774 MW; 56E4FF0226B58C92 CRC64;

Query Match 15.0%; Score 159.5; DB 5; Length 1253;
Best Local Similarity 27.4%; Pred. No. 0.19; Mismatches 75; Indels 27; Gaps 7;
Matches 57; Conservative 49;

QY 10 DLAGEENVLDREFLKNEL-DNVR--AQLSQDKKRDQYIIDTLRDTLEERNATVYS 65
DB 336 DLKSTQENVEDERVKRELEENVRRKEAELSSLSKLEDEQVLVSQLORKIKELQARIEE 395
QY 66 LQALGKAEMLCSTLKKOMKYLEQOODETKQAQEEAGRLRSKMKTMEQIELLSQLPVEY 125

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Db 396 LEELEAEARNARAKVEKQRAELNRELEBELGERLDEAGG-----ATSAQIELNKKRE-AEL 449
Qy 126 EEMIRDMGVGQSAVEQOLAVYCVSLKKEYENLKEARKASGEVADLRDLFSRSKLTQTVY 185
Db 450 LKIRRD-----EASLQHEAQTIALRKKHQD-----AANEMADQV-----DQLQKVK 492
Qy 186 SELDOAKLELKSAAQKDLQSAQDEKIMSUK 213
Db 493 SKSEKEKQQLRSEVEDLQALQIQTSHSKNK 520

RESULT 31
Q17042 PRELIMINARY; PRT; 1951 AA.
ID 017042
AC 017042;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Aequipecten irradians (Bay scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, CATCH (SMOOTH) ADDUCTOR;
RX MEDLINE=95108023; Pubmed=7809102;
RA Nyltroy L., Janoso A., Ochial Y., Graf L., Szent-Gyorgyi A.G.;
RT "Scallop striated and smooth muscle myosin heavy-chain isoforms are
RT produced by alternative RNA splicing from a single gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:12686-12690(1994).
DR EMBL: U09782; AAC46490.1; -
DR HSSP: P24733; IMDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; Myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR Pfam: PR00612; IQ_2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ_1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 1951 AA; 224253 MW; 1FDC3D7D691C1410 CRC64;

Query Match 15.0%; Score 159.5; DB 5; Length 1951;
Best Local Similarity 27.4%; Pred. No. 0.29;
Matches 57; Conservative 49; Mismatches 75; Indels 27; Gaps 7;

Qy 10 DLAGEENVLDREFLKNEL-DNVR---AQLSOKKEKRDQSVIITDLDTLERNAATVS 65
Db 1058 DLKSTQENVLELERYKRLLENVRKKEKESLSLSKLEDEONLVSQLRKKELOARIEE 1117
Qy 66 LQALGRAEMLCSTLKKOMKYLEOQODETKQAQEBAGRLRSKMTMEQIELLLOSQLEPV 125
Db 1118 LEELEAEARNARAKVEKQRAELNRELEBELGERLDEAGG-----ATSAQIELNKKRE-AEL 1171
Qy 126 EEMIRDMGVGQSAVEQOLAVYCVSLKKEYENLKEARKASGEVADLRDLFSRSKLTQTVY 185
Db 1172 LKIRRD-----EASLQHEAQTIALRKKHQD-----AANEMADQV-----DQLQKVK 1214
Qy 186 SELDOAKLELKSAAQKDLQSAQDEKIMSUK 213
Db 1215 SKSEKEKQQLRSEVEDLQALQIQTSHSKNK 1242

RESULT 32
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Q07569
ID 007569 PRELIMINARY; PRT; 2139 AA.
AC 007569; 002504;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
GN MHCA.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI:IMSS;
RX MEDLINE=93295430; Pubmed=8515774;
RA Raymond-Denise A., Sansonetti P., Guillen N.;
RT "Identification and characterization of a myosin heavy chain gene
RT (mhca) from the human parasitic pathogen Entamoeba histolytica.";
RL Mol. Biochem. Parasitol. 59:123-131(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI:IMSS;
RA Guillen N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: L03534; AAB48065.1; -
DR HSSP: P08799; IMND.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00612; IQ_2.
DR Pfam: PF00063; myosin_head; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00242; MYSC; 1.
SQ SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

Query Match 15.0%; Score 159.5; DB 5; Length 2139;
Best Local Similarity 24.0%; Pred. No. 0.32;
Matches 60; Conservative 49; Mismatches 96; Indels 45; Gaps 7;

Qy 5 NKLFFDL--AOEENVLDREFLKNELDNVRAQLSOKREKRDQVI-----ID 50
Db 1144 NKIEGDLRNAQRIKIELDEITKGA--DV-SQYLQKQKEEVSQAKMQEKEAIGNDVK 1200
Qy 51 TLRLTEERNATVYSLQALGKAEMLCSTLKKOMKYLEOQODETKQAQEBAGRLRSKKT 110
Db 1201 NKEKTIKKELEIQLSLOERLDETEVEKEDAEKKKEIK---EMKALQEBKENVESSKNS 1257
Qy 111 MEQIELLOSQLEPEVEEMIRDMGVGQSAVEQOLAVYCVSLKKEYENLKEARKASGEVADKL 170
Db 1258 TEKDKKKLELDNLQTKKLDMDTADNEKLUKAKAKLEQLNEVQDNHKEKAVADAELNKK 1317
Qy 171 R---KDLFSSRSKLQ-----TVSELDOAKLELKSAAQKDLQSA 205
Db 1318 KAQSDKELNSLKALEALTLAKASVESKNKDSENEKALSEIIDQANERKLKNIQADLRKA 1377
Qy 206 DKEIMSLKK 215
Db 1378 TADLQEANER 1387

RESULT 33
Q07380 PRELIMINARY; PRT; 1790 AA.
ID 007380
AC 007380; P89892;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 206.5 KDA PROTEIN YDL058W.
GN USO1 OR YDL058W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bloeker H., Brandt P.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 274106; CA98621.1; -;
 DR EMBL; 274105; CA98620.1; -;
 DR SGD; S0002216; US01.
 DR InterPro: IPR002017; Spectrin.
 SQ SEQUENCE 1790 AA; 206450 MW; 90062544F55A52EE CRC64;

Query Match 14.9%; Score 159; DB 3; Length 1790;
 Best Local Similarity 23.7%; Pred. No. 0.29;
 Matches 61; Conservative 57; Mismatches 85; Indels 54; Gaps 9;

QY 1 RTITKLEFPDLAQ---EEENVLDREFLK-----NELDNVRAQLSOKDKKKDSQVI 48
 Db 1369 RRLNEGSSITIOEYSEKINTELEDIRLQENENELKAEIDMTRESEL-EKVSLSND---- 1423
 QY 49 IDTLDTLEERNATVVSIOQAL-----GKAEMLSLTKQMKYLBQODETKQAQEE 100
 Db 1424 -----ELLEKONTIKSLQDELSTKDKITTRNDEKLTSTERNKRDLESLEKQLRAQDS 1478
 QY 101 AGRLSKMKTMEOILLLQSLPEVEEMIRDMGVGSAVE---OLAVYCVSLKKEYEVL 156
 Db 1479 KAKVEGLKLTLEESSEKAELEKSEKMKKL---ESTIESMETELKSSMETIRKSDKL 1535
 QY 157 KEARASGEVADKLR-----KDLFSSRSKIQTVY---SELDAQKLELKSQ 199
 Db 1536 EOSKSSAEEDIKNLQHEKSDLSIRINESEKIDIEELKSLRIEAKSGSELETKQELNNAQ 1595
 QY 200 KDLOSADKEIMSLKKKL 216
 Db 1596 EKIRINAEENTVYLSKL 1612

RESULT 34
 Q9TV61 PRELIMINARY; PRT: 1939 AA.
 AC Q9TV61;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN 2X.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LANDRACE; TISSUE=SKLETAL MUSCLE;
 RA Chikuni K., Tanabe R., Muroya S., Nakajima I.;
 RT "Differences in molecular structure among the porcine myosin heavy
 chain-2a, -2x, and -2b isoforms.";
 RL Meat Sci. 57:311-317(2001).
 DR EMBL; AB025262; BAA82146.1; -;
 DR HSSP; P13538; 2MVS.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF02736; myosin_N; 1.
 DR Pfam; PF01576; myosin_tail; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PSS0096; IQ; 1.
 SQ SEQUENCE 1939 AA; 223172 MW; B702ADB599602ECB CRC64;

Query Match 14.9%; Score 159; DB 6; Length 1939;
 Best Local Similarity 24.2%; Pred. No. 0.31;
 Matches 55; Conservative 48; Mismatches 80; Indels 44; Gaps 7;

QY 24 LKNELDNVRAQLSOKDKERDSQVIITDLRDLERNATVVSIOQALGKAEMLSLTKQ 83
 Db 1207 LGEQIDNLDNRVQKLEKESEKMKMEIDLASNME-----TVSKAKGNLEKMKRTLEDQ 1259
 QY 84 MKYLBQODETK-----QAOEEAGRL-----RSKMKTMEOIELL 117
 Db 1260 LSELKTEEEQORLINDLTAORARLQTESGEYSRQLDEKDTLVLSRKQAKFTQOIEEL 1319
 QY 118 LOSQLPEVEEMIRDMGVGSAVEOLAVYCVSLKKEYEMLKEARKASGEVADLRKDRSS 177
 Db 1320 KR-----QLEEEIKAKSALAHAVQSSRHQCDLREQYEEQEKAKELQRAMSKANSEVAMQ 1375
 QY 178 RSKIQT---VYSELDAQKLELSAQDKLOSADKEIMSLKKKLTMQ 220
 Db 1376 RTKYETDAIQRTPEELEAKKKL--AQR-LQDAEEHVAVMKCASTLE 1419

RESULT 35
 Q26079 PRELIMINARY; PRT: 1941 AA.
 AC Q26079;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 OS Placopecten magellanicus (Sea scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
 OC Pectinoidea; Pectinidae; Placopecten.
 NCBI_TaxID=6577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKLETAL MUSCLE;
 RA Perreault-Micale C., Kalabokis V., Nyitrai L., Szent-Gyorgyi A.G.;
 RT "Sequence variations in the surface loop near the nucleotide binding
 site modulate the ATP turnover rates of molluscan myosins.";
 RL J. Muscle Res. Cell Motil. 0:0-0(1996).
 DR EMBL; U59294; AAB03660.1; -;
 DR HSSP; P24733; IMDC.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF02736; myosin_N; 1.
 DR Pfam; PF01576; myosin_tail; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PSS0096; IQ; 1.
 SQ SEQUENCE 1941 AA; 223243 MW; E2AD1637FFDB8127 CRC64;

Query Match 14.9%; Score 158.5; DB 5; Length 1941;
 Best Local Similarity 27.5%; Pred. No. 0.33;
 Matches 56; Conservative 49; Mismatches 72; Indels 27; Gaps 7;
 QY 5 NKLFFDLAQEEENVLDREFLKNEI-DNVR---AQLSOKDKERDSQVIITDLRDTLEERN 60
 Db 1053 SKVEDLTKSTQENVEDLERVARELEENVRKREAEITTLNSKLEDEQNLVSOLOQRKRELQ 1112
 QY 61 ATVVSIOQALGKAEMLSLTKQMKYLBQODETKQAQEEAGRLSKMKTMEOIELLLQS 120
 Db 1113 ARIELEELERNAERNAKSVKQRAELRLEELGEERLDEAGG---ATSAQLELNKKR 1167
 QY 121 QLPEVEEMIRDMGVGSAVEOLAVYCVSLKKEYEMLKEARKASGEVADKLKDLFSSRSK 180

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Db 1168 E-ABLTKIRRLD---EEASLQHEAQAISAIRKHOD-----AANEMADQV-----DQ 1209
QY 181 LQTVYSELDQAKLELKSQAKDLOS 204
Db 1210 LQVKVSKLEKDKDKREMDLES 1233

RESULT 36
Q91520 PRELIMINARY; PRT: 786 AA.
AC Q91520;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE SKELETAL MYOSIN HEAVY CHAIN (FRAGMENT).
OS Thunnus thynnus (Bluefin tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
NCBI_TaxId=8237;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RA Hirayama Y., Watabe S.;
RT "cDNA cloning of bluefin tuna skeletal muscle myosin heavy chain.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D85138; BAI2730.1; -.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
FT NON_TER
SQ SEQUENCE 786 AA; 90580 MW; 0279F714CA649A10 CRC64;

Query Match 14.7%; Score 156.5; DB 13; Length 786;
Best Local Similarity 24.0%; Pred. No. 0.18;
Matches 63; Conservative 48; Mismatches 91; Indels 61; Gaps 9;

QY 6 KLFDLAQEEENVLDREF-----LKNELDNVRAQLSOKDKERSQVIID 50
Db 23 KLRRDL---EESTLQHEATSALRKQADVAELEQIDNLRVKKLEKSEYKMEID 79
QY 51 TLRLTLEERNATVVSLOALGKAEMLCSTLKQKYLEQODETRKQAOEEGRLSKMKT 110
Db 80 DLSSNME-----AVAKSKGNLEKMCRTIEDQLSELKAKNDEHYROLNDLNGQARLQT 132
QY 111 -----MEQIEL--LLOSQLP-----EVEEMIRDMGVGQSAVEQLAVYCVS 148
Db 133 ENGFSROIEKDALVSOQLTRGQAYTQOIELKRHIEELKAKNALAHVQSAHDCDL 192
QY 149 LKKEYENLKEAR-----KASGEVAD--KLRRDLFSSRSKLTQTVYSELDQAKLELS 197
Db 193 LREQYEEQEAKEGLOKMSKANSEVAQWRTYETDAIQRTPELEBAKKLAQ--RLQD 249
QY 198 AQKDLQSAKDEIMSLKKKLTMLQ 220
Db 250 AEESIEAVNSKASLEKTRQLQ 272

RESULT 37
Q22276 PRELIMINARY; PRT: 1138 AA.
AC Q22276; Q22294;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE T07C4.10 PROTEIN.
GN T07C4.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;

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OC Rhabdilitidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Buck D., Berks M.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: 248055; CAA88136.1; -.
DR EMBL: 229443; CAA88136.1; JOINED.
DR EMBL: 229443; CAA82580.1; -.
DR EMBL: 248055; CAA82580.1; JOINED.
SQ SEQUENCE 1138 AA; 132785 MW; DF16C5F5A1B1155E CRC64;

Query Match 14.7%; Score 156.5; DB 5; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.25;
Matches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;

QY 1 RTIINKLFFDLAQEEENVLDREF-LKNELDNVRAQL-----SOKDKERK 43
Db 544 KTIYKENVY-LSESKQVLESEINLKNELDDEMAVKLRNSQHVAAGLNKISEEKRRRKQ 602
QY 44 DSOYIITLRLTLEERNATVVSLOALGKAEML--CSTLKQKYLEQODETRKQAOEEA 101
Db 603 DADV-----TRLDEQNKLT--LREADSSELLLEEVQKGRKREIDHLRQQLAHOSSEAGSV 654
QY 102 GLRKSMMKMTMEQIELLLOSQLPVEVEEMIIPMGVQSAVEQLAVYCVSLKKEYENLKEARK 161
Db 655 GQLQQALESHPREYLLQLLELRYMKMERD-----LDGRIEYITSEA 697
QY 162 ASGEVADKLRRDLFSSRSKLTQTVYSELDQAKLELSAQKDLQSAKDEIMSLKKRL 216
Db 698 AANLELRLRKDTAEQKEKLEA-----MEWEARSKDLELAD-----LTRKL 738

RESULT 38
Q907E3 PRELIMINARY; PRT: 1940 AA.
AC Q907E3;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Pecten maximus (King scallop) (P1) (prim's clam).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Pectinoida;
OC Pectinoidae; Pectinidae; Pecten.
OX NCBI_TaxId=6579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADDUCTOR MUSCLE;
RA Jones D.P., Patel H., Chantler P.D.;
RT "Primary structure of myosin from the striated adductor muscle of the
Atlantic scallop, Pecten maximus.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF134172; AAD52842.1; -.
DR HSP: P24733; IWDG.
DR InterPro: IPR000048; IO.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR InterPro: IPR002928; myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR Pfam: PF00612; IO; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IO; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PSS0096; IO; 1.
SQ SEQUENCE 1940 AA; 223141 MW; A3D09DECBEB16F90 CRC64;

Query Match 14.7%; Score 156.5; DB 5; Length 1940;

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Best Local Similarity 27.6%; Pred. No. 0.43;
Matches 55; Conservative 47; Mismatches 70; Indels 27; Gaps 7;

OY 10 DLAGEENVLDREFLNEL-DNVR---AQLSOKDKERDSQYIITLRLTLEERNATVVS 65
DB 1058 DLKSTQENVEDERKRELEENVRKREAEISTLNKSLDEQNLVSQLOKRVKELQARIEE 1117
OY 66 LQALGKAKMLCSTLKKOMKYLEQOODETKQAQEAAGRLSKMKTMEOIELLOSQLEPV 125
DB 1118 LEEELAEARNNAKVEKQRAELNRELEGERLDEAG-----ATSAQELNKKRE-AEL 1171
OY 126 EEMIRDMGVGSAVQOLAVYCVSLKKEYENLKEARRKAGEVADKLKDLFSSRSKLQTVY 185
DB 1172 LKIRIDL---EASLQHEAQSALRKKHOD-----AANEMADQY-----DOLQKVK 1214
OY 186 SELDOAKLELKSQKDLOS 204
DB 1215 SKLEKDKKDKREMDLES 1233

RESULT 39

OY 091ME7 PRELIMINARY; PRT; 959 AA.
AC 091ME7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SIMILAR TO TRANSCYTOSIS ASSOCIATED PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE, AND RETINA;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016069; AAH16069.1;
SQ SEQUENCE 959 AA; 106983 MW; 2C05DC35E899D81C CRC64;

Query Match 14.6%; Score 155.5; DB 11; Length 959;
Best Local Similarity 19.5%; Pred. No. 0.25;
Matches 64; Conservative 52; Mismatches 81; Indels 131; Gaps 8;

OY 15 EENVLDREFLK--NELDNV--RAQLSOKDKERDSQYIITLRLTLEERNATVVSLOAL 70
DB 605 EYMTDHEFTLVKLEBEGVITKAIKSSSEDDKKEEV-----KTLLEQHDNIVTHYKMTI 659
OY 71 GKAEMLCSTLKKOMKYLEQODE---TKQAQ----- 98
DB 660 REQDLQLEELKQOYSTLCQNBQLOTAVTQQAQSQLOQHKDDYNLLKVLGKDNHQSNG 719
OY 99 -----EAGRLRSKMKTMEOIELLOSQLEPEVEMIRDMGVGSA--VEQOLAVYC 146
DB 720 DGAQVNGIQPEISRLREIEIELKSQALLOGLAELKDSLLENLKSQASGMSQASATC 779
OY 147 ----- 146
DB 780 PPRDPEOVAELKQELTALKSOLCSOSLEITRLQTEENCELLQRAETLAKSVPEGESEHVS 839
OY 147 -----VSLKKEYENLKEARRKAGEVADKLKDLFSSRSKLQTVYSELDOAKLEL 195
DB 840 AAKTTDVEGRSLALLQETKELKNEKALSEERTAIQKQDSSNSTIATLQTEKDKLDLEV 899
OY 196 KSAQKD-----LOSADKETMSLKKL 216
DB 900 TDSKKEQDDLVLADQDKILSLSKL 927

RESULT 40
P92021 PRELIMINARY; PRT; 1164 AA.

AC P92021;
DT 01-NOV-1997 (Tremblrel. 03, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE T10G3.5 PROTEIN.
GN T10G3.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderiinae; Caenorhabditis.
OX NCBI_TaxID=6239;

RN [1]
RP SEQUENCE FROM N.A.
RA Burton J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81118; CAB03330.1;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000822; ZnF-C2H2.
DR InterPro; IPR000306; ZnF_FYVE.
DR Pfam; PF01363; FYVE.1.
DR SMART; SM00064; FYVE.1.
DR SMART; SM00355; ZnF_C2H2.1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2.1; UNKNOWN.1.
SQ SEQUENCE 1164 AA; 135041 MW; 0C8C438680E755C3 CRC64;

Query Match 14.6%; Score 155.5; DB 5; Length 1164;
Best Local Similarity 24.8%; Pred. No. 0.3;
Matches 52; Conservative 51; Mismatches 80; Indels 27; Gaps 6;

OY 22 EFLKNELDNVRRAQLSOKDK-----EKRSQYIITLRLTLEERNATV 63
DB 700 EELKQVQKVENSEISEKQOEVENLMAEMRKDEAKMKTRDFEFQOMLRNQNDEASSTL 759
OY 64 VSLQALGKAKMLCSTLKKOMKYLEQODETKQAQEAAGRLSKMKTMEOIELLOSQLP 123
DB 760 KSVQOLKREKETSQGEENQLISVQLELELKTVEERL--IRSEEEKTOEIEKLSAVTA 817
OY 124 EVEEMIRDMGVGSAVQOLAVYCVSLKKEYENLKEARRKAGEVADKLKDLFSSRSKLQ 183
DB 818 TTQE--RDELTAAT--ESLRTCEENLNSKIOSIESRRHAEKGSSENLERMITKSRLE- 872
OY 184 VYSELDOAKLELKSQAKDQASADREIMSLK 213
DB 873 --KDIERESTIQSIQEALEFKNDIEESLK 900

Search completed: September 4, 2002, 16:16:02
Job time: 1486 sec

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